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CLAIMS

1. A gram-positive microorganism having a mutation or deletion of part or all of the nucleic acid encoding MP, said mutation or deletion resulting in the inactivation of the MP proteolytic activity.
2. The gram-positive microorganism according to Claim 1 that is a member of the family *Bacillus*.
3. The microorganism according to Claim 2 wherein the member is selected from the group consisting of *B. subtilis*, *B. licheniformis*, *B. lentus*, *B. brevis*, *B. stearothermophilus*, *B. alkalophilus*, *B. amyloliquefaciens*, *B. coagulans*, *B. circulans*, *B. lautus* and *Bacillus thuringiensis*.
4. The microorganism of Claim 3 wherein the *Bacillus* is *Bacillus subtilis* and the MP has the amino acid sequence as shown in Figure 1A-1O.
5. The microorganism of Claim 3 wherein the *Bacillus* is *Bacillus subtilis* and the MP has the amino acid sequence encoding by the MP nucleic acid found about 2248 kb from the point of origin.
6. The microorganism of Claims 1, 2, 3, 4 or 5 wherein said microorganism comprises nucleic acid encoding a heterologous protein.
7. The microorganism of Claims 1, 2, 3, 4 or 5 wherein said microorganism comprises nucleic acid encoding a homologous protein.
8. The microorganism of Claim 6 wherein said heterologous protein is selected from the group consisting of hormone, enzyme, growth factor and cytokine.
9. The microorganism of Claim 8 wherein said heterologous protein is an enzyme.

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10. The microorganism of Claim 9 wherein said enzyme is selected from the group consisting of a proteases, carbohydrases, and lipases; isomerases such as racemases, epimerases, tautomerases, or mutases; transferases, kinases and phosphatases.
11. A cleaning composition comprising a gram positive microorganism MP.
12. The cleaning composition of Claim 11 wherein the gram positive microorganism is a *Bacillus*.
13. The cleaning composition of Claim 11 wherein the MP has the amino acid sequence as shown in Figures 1A-1O.
14. The cleaning composition of Claim 11 wherein the MP has the amino acid sequence encoding by MP nucleic acid found about 2248 kilobases from the point of origin in *Bacillus subtilis*.
15. The cleaning composition of Claim 12 wherein the gram positive microorganism is selected from the group consisting of *B. subtilis*, *B. licheniformis*, *B. lentus*, *B. brevis*, *B. stearothermophilus*, *B. alkalophilus*, *B. amyloliquefaciens*, *B. coagulans*, *B. circulans*, *B. lautus* and *Bacillus thuringiensis*.
16. A cleaning composition comprising a metalloprotease having at least 80% homology with the amino acid having the sequence shown in Figures 1A-1O.
17. An animal feed comprising a metalloprotease comprising the amino acid having the sequence shown in Figures 1A-1O.
18. An animal feed comprising a metalloprotease having at least 80% homology with the amino acid shown in Figures 1A-1O.
19. A composition for the treatment of a textile comprising a metalloprotease comprising the amino acid having the sequence as shown in Figures 1A-1O.

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20. A composition for the treatment of a textile comprising a metalloprotease having at least 80% homology with the amino acid having the sequence as shown in Figures 1A-1O.
21. An expression vector comprising nucleic acid encoding a gram-positive MP.
22. The expression vector of Claim 21 wherein the nucleic acid encodes *Bacillus subtilis* MP.
23. The expression vector of Claim 21 wherein the nucleic acid is a *Bacillus subtilis* MP polynucleotide homolog.
24. A host cell comprising an expression vector according to Claims 21, 22 or 23.
25. A method for detecting a gram-positive microorganism MP, comprising the steps of
- (a) hybridizing gram-positive microorganism nucleic acid under low stringency conditions to a probe, wherein the probe comprises part or all of the nucleic acid sequence shown in Figures 1A-1O; and
 - (b) isolating gram-positive nucleic acid which hybridizes to said probe.

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